

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/559, 639
Source: IFWP
Date Processed by STIC: 12/16/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENT IN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/559,639

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> ~~Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.~~
 ~~Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.~~
 ~~(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules))~~

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,639

TIME: 15:46:54

Input Set : D:\Sequence_Listings_16033US_ST25_txt.TXT

Output Set: N:\CRF4\12162005\J559639.raw

3 <110> APPLICANT: Ben-Yehuda, Dina
 4 Ashhab, Yaqoub
 5 Nachmias, Boaz
 7 <120> TITLE OF INVENTION: Livin-derived peptides, compositions and uses thereof
 9 <130> FILE REFERENCE: 16033/US/03
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/559,639
 C--> 11 <141> CURRENT FILING DATE: 2005-12-02
 11 <150> PRIOR APPLICATION NUMBER: IL 156263
 12 <151> PRIOR FILING DATE: 2003-06-02
 14 <150> PRIOR APPLICATION NUMBER: PCT/IL2004/000461
 15 <151> PRIOR FILING DATE: 2004-05-31
 17 <160> NUMBER OF SEQ ID NOS: 11
 19 <170> SOFTWARE: PatentIn version 3.3
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 246
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Homo sapiens
 26 <400> SEQUENCE: 1
 28 Gly Gln Ile Leu Gly Gln Leu Arg Pro Leu Thr Glu Glu Glu Glu Glu
 29 1 5 10 15
 32 Glu Gly Ala Gly Ala Thr Leu Ser Arg Gly Pro Ala Phe Pro Gly Met
 33 20 25 30
 36 Gly Ser Glu Glu Leu Arg Leu Ala Ser Phe Tyr Asp Trp Pro Leu Thr
 37 35 40 45
 40 Ala Glu Val Pro Pro Glu Leu Leu Ala Ala Ala Gly Phe Phe His Thr
 41 50 55 60
 44 Gly His Gln Asp Lys Val Arg Cys Phe Phe Cys Tyr Gly Gly Leu Gln
 45 65 70 75 80
 48 Ser Trp Lys Arg Gly Asp Asp Pro Trp Thr Glu His Ala Lys Trp Phe
 49 85 90 95
 52 Pro Ser Cys Gln Phe Leu Leu Arg Ser Lys Gly Arg Asp Phe Val His
 53 100 105 110
 56 Ser Val Gln Glu Thr His Ser Gln Leu Leu Gly Ser Trp Asp Pro Trp
 57 115 120 125
 60 Glu Glu Pro Glu Asp Ala Ala Pro Val Ala Pro Ser Val Pro Ala Ser
 61 130 135 140
 64 Gly Tyr Pro Glu Leu Pro Thr Pro Arg Arg Glu Val Gln Ser Glu Ser
 65 145 150 155 160
 68 Ala Gln Glu Pro Gly Gly Val Ser Pro Ala Glu Ala Gln Arg Ala Trp
 69 165 170 175
 72 Trp Val Leu Glu Pro Pro Gly Ala Arg Asp Val Glu Ala Gln Leu Arg
 73 180 185 190
 76 Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Leu Asp Arg Ala Val

Does Not Comply
Corrected Diskette Needed
(pg-5)

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Input Set : D:\Sequence_Listings_16033US_ST25_txt.TXT

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80 Ser Ile Val Phe Val Pro Cys Gly His Leu Val Cys Ala Glu Cys Ala
81          210          215          220
84 Pro Gly Leu Gln Leu Cys Pro Ile Cys Arg Ala Pro Val Arg Ser Arg
85 225          230          235          240
88 Val Arg Thr Phe Leu Ser
89          245
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 228
94 <212> TYPE: PRT
95 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 2
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100 1          5          10          15
103 Glu Gly Ala Gly Ala Thr Leu Ser Arg Gly Pro Ala Phe Pro Gly Met
104          20          25          30
107 Gly Ser Glu Glu Leu Arg Leu Ala Ser Phe Tyr Asp Trp Pro Leu Thr
108          35          40          45
111 Ala Glu Val Pro Pro Glu Leu Ala Ala Ala Gly Phe Phe His Thr
112          50          55          60
115 Gly His Gln Asp Lys Val Arg Cys Phe Phe Cys Tyr Gly Gly Leu Gln
116 65          70          75          80
119 Ser Trp Lys Arg Gly Asp Asp Pro Trp Thr Glu His Ala Lys Trp Phe
120          85          90          95
123 Pro Ser Cys Gln Phe Leu Leu Arg Ser Lys Gly Arg Asp Phe Val His
124          100          105          110
127 Ser Val Gln Glu Thr His Ser Gln Leu Leu Gly Ser Trp Asp Pro Trp
128          115          120          125
131 Glu Glu Pro Glu Asp Ala Ala Pro Val Ala Pro Ser Val Pro Ala Ser
132          130          135          140
135 Gly Tyr Pro Glu Leu Pro Thr Pro Arg Arg Glu Val Gln Ser Glu Ser
136 145          150          155          160
139 Ala Gln Glu Pro Gly Ala Arg Asp Val Glu Ala Gln Leu Arg Arg Leu
140          165          170          175
143 Gln Glu Glu Arg Thr Cys Lys Val Cys Leu Asp Arg Ala Val Ser Ile
144          180          185          190
147 Val Phe Val Pro Cys Gly His Leu Val Cys Ala Glu Cys Ala Pro Gly
148          195          200          205
151 Leu Gln Leu Cys Pro Ile Cys Arg Ala Pro Val Arg Ser Arg Val Arg
152          210          215          220
155 Thr Phe Leu Ser
156 225
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 298
161 <212> TYPE: PRT
162 <213> ORGANISM: Homo sapiens
164 <400> SEQUENCE: 3
166 Met Gly Pro Lys Asp Ser Ala Lys Cys Leu His Arg Gly Pro Gln Pro
167 1          5          10          15

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Input Set : D:\Sequence_Listings_16033US_ST25_txt.TXT

Output Set: N:\CRF4\12162005\J559639.raw

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170 Ser His Trp Ala Ala Gly Asp Gly Pro Thr Gln Glu Arg Cys Gly Pro
171          20          25          30
174 Arg Ser Leu Gly Ser Pro Val Leu Gly Leu Asp Thr Cys Arg Ala Trp
175          35          40          45
178 Asp His Val Asp Gly Gln Ile Leu Gly Gln Leu Arg Pro Leu Thr Glu
179          50          55          60
182 Glu Glu Glu Glu Glu Gly Ala Gly Ala Thr Leu Ser Arg Gly Pro Ala
183 65          70          75          80
186 Phe Pro Gly Met Gly Ser Glu Glu Leu Arg Leu Ala Ser Phe Tyr Asp
187          85          90          95
190 Trp Pro Leu Thr Ala Glu Val Pro Pro Glu Leu Leu Ala Ala Ala Gly
191          100         105         110
194 Phe Phe His Thr Gly His Gln Asp Lys Val Arg Cys Phe Phe Cys Tyr
195          115         120         125
198 Gly Gly Leu Gln Ser Trp Lys Arg Gly Asp Asp Pro Trp Thr Glu His
199          130         135         140
202 Ala Lys Trp Phe Pro Ser Cys Gln Phe Leu Leu Arg Ser Lys Gly Arg
203 145          150          155          160
206 Asp Phe Val His Ser Val Gln Glu Thr His Ser Gln Leu Leu Gly Ser
207          165          170          175
210 Trp Asp Pro Trp Glu Glu Pro Glu Asp Ala Ala Pro Val Ala Pro Ser
211          180          185          190
214 Val Pro Ala Ser Gly Tyr Pro Glu Leu Pro Thr Pro Arg Arg Glu Val
215          195          200          205
218 Gln Ser Glu Ser Ala Gln Glu Pro Gly Gly Val Ser Pro Ala Glu Ala
219          210          215          220
222 Gln Arg Ala Trp Trp Val Leu Glu Pro Pro Gly Ala Arg Asp Val Glu
223 225          230          235          240
226 Ala Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Leu
227          245          250          255
230 Asp Arg Ala Val Ser Ile Val Phe Val Pro Cys Gly His Leu Val Cys
231          260          265          270
234 Ala Glu Cys Ala Pro Gly Leu Gln Leu Cys Pro Ile Cys Arg Ala Pro
235          275          280          285
238 Val Arg Ser Arg Val Arg Thr Phe Leu Ser
239          290          295
242 <210> SEQ ID NO: 4
243 <211> LENGTH: 280
244 <212> TYPE: PRT
245 <213> ORGANISM: Homo sapiens
247 <400> SEQUENCE: 4
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250 1          5          10          15
253 Ser His Trp Ala Ala Gly Asp Gly Pro Thr Gln Glu Arg Cys Gly Pro
254          20          25          30
257 Arg Ser Leu Gly Ser Pro Val Leu Gly Leu Asp Thr Cys Arg Ala Trp
258          35          40          45
261 Asp His Val Asp Gly Gln Ile Leu Gly Gln Leu Arg Pro Leu Thr Glu
262          50          55          60

```

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```

265 Glu Glu Glu Glu Glu Gly Ala Gly Ala Thr Leu Ser Arg Gly Pro Ala
266 65                               70                               75                               80
269 Phe Pro Gly Met Gly Ser Glu Glu Leu Arg Leu Ala Ser Phe Tyr Asp
270                               85                               90                               95
273 Trp Pro Leu Thr Ala Glu Val Pro Pro Glu Leu Leu Ala Ala Ala Gly
274                               100                              105                              110
277 Phe Phe His Thr Gly His Gln Asp Lys Val Arg Cys Phe Phe Cys Tyr
278                               115                              120                              125
281 Gly Gly Leu Gln Ser Trp Lys Arg Gly Asp Asp Pro Trp Thr Glu His
282                               130                              135                              140
285 Ala Lys Trp Phe Pro Ser Cys Gln Phe Leu Leu Arg Ser Lys Gly Arg
286 145                               150                              155                              160
289 Asp Phe Val His Ser Val Gln Glu Thr His Ser Gln Leu Leu Gly Ser
290                               165                              170                              175
293 Trp Asp Pro Trp Glu Glu Pro Glu Asp Ala Ala Pro Val Ala Pro Ser
294                               180                              185                              190
297 Val Pro Ala Ser Gly Tyr Pro Glu Leu Pro Thr Pro Arg Arg Glu Val
298                               195                              200                              205
301 Gln Ser Glu Ser Ala Gln Glu Pro Gly Ala Arg Asp Val Glu Ala Gln
302                               210                              215                              220
305 Leu Arg Arg Leu Gln Glu Arg Thr Cys Lys Val Cys Leu Asp Arg
306 225                               230                              235                              240
309 Ala Val Ser Ile Val Phe Val Pro Cys Gly His Leu Val Cys Ala Glu
310                               245                              250                              255
313 Cys Ala Pro Gly Leu Gln Leu Cys Pro Ile Cys Arg Ala Pro Val Arg
314                               260                              265                              270
317 Ser Arg Val Arg Thr Phe Leu Ser
318                               275                              280

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321 <210> SEQ ID NO: 5

322 <211> LENGTH: 27

323 <212> TYPE: DNA

324 <213> ORGANISM: Artificial Sequence

326 <220> FEATURE:

327 <223> OTHER INFORMATION: Primer for site-directed mutagenesis

329 <400> SEQUENCE: 5

330 ggggaattct ggtcagagcc agtgttc

27

333 <210> SEQ ID NO: 6

334 <211> LENGTH: 24

335 <212> TYPE: DNA

336 <213> ORGANISM: Artificial Sequence

338 <220> FEATURE:

339 <223> OTHER INFORMATION: Primer for site-directed mutagenesis

341 <400> SEQUENCE: 6

342 gggggatccg gagcccactc tgca

24

345 <210> SEQ ID NO: 7

346 <211> LENGTH: 18

347 <212> TYPE: DNA

348 <213> ORGANISM: Artificial Sequence;

350 <220> FEATURE:

RAW SEQUENCE LISTING

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,639

TIME: 15:46:54

Input Set : D:\Sequence_Listings_16033US_ST25_txt.TXT

Output Set: N:\CRF4\12162005\J559639.raw

351 <223> OTHER INFORMATION: Mega-primer to introduce mutation D52E
353 <400> SEQUENCE: 7
354 cgtggaaggg cagatcct 18
357 <210> SEQ ID NO: 8
358 <211> LENGTH: 19
359 <212> TYPE: DNA
360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:
363 <223> OTHER INFORMATION: Mega-primer to introduce mutation D238E
365 <400> SEQUENCE: 8
366 ccaggaagt agaggcgca 19
369 <210> SEQ ID NO: 9
370 <211> LENGTH: 41
371 <212> TYPE: DNA
372 <213> ORGANISM: Artificial Sequence
374 <220> FEATURE:
375 <223> OTHER INFORMATION: Primer to construct cleavage fragment
377 <400> SEQUENCE: 9
378 ggggaattca gtgttcctc catggggcag atcctgggcc a 41
381 <210> SEQ ID NO: 10
382 <211> LENGTH: 26
383 <212> TYPE: DNA
384 <213> ORGANISM: Artificial Sequence
386 <220> FEATURE:
387 <223> OTHER INFORMATION: Livin-Exp-F
389 <400> SEQUENCE: 10
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393 <210> SEQ ID NO: 11
394 <211> LENGTH: 27
395 <212> TYPE: DNA
396 <213> ORGANISM: Artificial Sequence
398 <220> FEATURE:
399 <223> OTHER INFORMATION: Livin-Exp-R
401 <400> SEQUENCE: 11
402 ggcaaagctt ctaggacagg aaggtgc 27

Invalid Response.
What is the source of
genetic material? Pls see
glen #11 on 26
error summary sheet.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/559,639

DATE: 12/16/2005

TIME: 15:46:55

Input Set : D:\Sequence_Listings_16033US_ST25_txt.TXT

Output Set: N:\CRF4\12162005\J559639.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date